

Gene	Protein-or-Domain	Score	E-Value	COG-ID	Function-Description	Code
<b>Functional-Categories:</b>						
CL16430.Contig2_tangwq	ECU11g0660	87.4	6e-18	COG0639	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	T Signal transduction mechanisms ;
CL16430.Contig1_tangwq	SPBC16H5.07c	87.0	7e-18	COG0639	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	T Signal transduction mechanisms ;
Unigene3118_tangwq	ECU04g0700	87.0	7e-18	COG0639	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	T Signal transduction mechanisms ;
Unigene3112_tangwq	SPAC823.15	85.9	2e-17	COG0639	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	T Signal transduction mechanisms ;
Unigene42182_tangwq	SPAC22H10.04	81.6	3e-16	COG0639	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	T Signal transduction mechanisms ;
Unigene4496_tangwq	YDL134c	80.9	5e-16	COG0639	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	T Signal transduction mechanisms ;
Unigene41350_tangwq	YDL188c	80.5	7e-16	COG0639	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	T Signal transduction mechanisms ;
CL1677.Contig2_tangwq	MT3990	57.0	4e-07	COG0455	ATPases involved in chromosome partitioning	D Cell cycle control, cell division, chromosome partitioning ;
CL1677.Contig1_tangwq	Rv2839c	56.6	5e-07	COG0532	Translation initiation factor 2 (IF-2; GTPase)	J Translation, ribosomal structure and biogenesis ;
CL1484.Contig1_tangwq	MT2905	56.6	5e-07	COG0532	Translation initiation factor 2 (IF-2; GTPase)	J Translation, ribosomal structure and biogenesis ;
Unigene55710_tangwq	Rv0171	55.8	8e-07	COG1463	ABC-type transport system involved in resistance to organic solvents, periplasmic component	Q Secondary metabolites biosynthesis, transport and catabolism ;
Unigene62483_tangwq	MT0180	55.8	8e-07	COG1463	ABC-type transport system involved in resistance to organic solvents, periplasmic component	Q Secondary metabolites biosynthesis, transport and catabolism ;
Unigene4416_tangwq	Cgl1939	54.3	2e-06	COG0532	Translation initiation factor 2 (IF-2; GTPase)	J Translation, ribosomal structure and biogenesis ;
CL9563.Contig1_tangwq	ECU05g0070_2	216	2e-55	COG1752	Predicted esterase of the alpha-beta hydrolase superfamily	R General function prediction only ;
Unigene63419_tangwq	YML059c_2	199	4e-50	COG1752	Predicted esterase of the alpha-beta hydrolase superfamily	R General function prediction only ;
CL1484.Contig2_tangwq	SPCC4B3.04c_1	187	2e-46	COG0664	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	T Signal transduction mechanisms ;
CL1484.Contig3_tangwq	SPCC4B3.04c_2	185	8e-46	COG1752	Predicted esterase of the alpha-beta hydrolase superfamily	R General function prediction only ;
Unigene78492_tangwq	lin0592	67.8	5e-12	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)	U Intracellular trafficking, secretion, and vesicular transport ;
Unigene67266_tangwq	Cj0942c	65.1	3e-11	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)	U Intracellular trafficking, secretion, and vesicular transport ;
Unigene67265_tangwq	jhp0723	64.3	5e-11	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)	U Intracellular trafficking, secretion, and vesicular transport ;
Unigene67264_tangwq	CT701	63.5	9e-11	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)	U Intracellular trafficking, secretion, and vesicular transport ;
Unigene67263_tangwq	HP0786	63.2	1e-10	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)	U Intracellular trafficking, secretion, and vesicular transport ;
Unigene67262_tangwq	SPy1805	60.8	6e-10	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)	U Intracellular trafficking, secretion, and vesicular transport ;
Unigene42419_tangwq	SP1702	60.8	6e-10	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)	U Intracellular trafficking, secretion, and vesicular transport ;
Unigene73614_tangwq	CPn0841	60.1	1e-09	COG0653	Preprotein translocase subunit SecA (ATPase, RNA helicase)	U Intracellular trafficking, secretion, and vesicular transport ;
Unigene5532_tangwq	Rv3876	47.4	8e-06	COG0455	ATPases involved in chromosome partitioning	D Cell cycle control, cell division, chromosome partitioning ;
CL9563.Contig5_tangwq	MT3990	47.4	8e-06	COG0455	ATPases involved in chromosome partitioning	D Cell cycle control, cell division, chromosome partitioning ;
CL9563.Contig4_tangwq	NMB0059	76.3	2e-14	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain	O Posttranslational modification, protein turnover, chaperones ;
Unigene71813_tangwq	NMA0209	76.3	2e-14	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain	O Posttranslational modification, protein turnover, chaperones ;
Unigene70273_tangwq	CT341	75.1	4e-14	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain	O Posttranslational modification, protein turnover, chaperones ;
Unigene68912_tangwq	CPn0032	74.7	5e-14	COG0484	DnaJ-class molecular chaperone with C-terminal Zn finger domain	O Posttranslational modification, protein turnover, chaperones ;
Unigene66832_tangwq	all10438_1	47.0	8e-06	COG0515	Serine/threonine protein kinase RTKL	General function prediction only ; Signal transduction mechanisms ; Transcription ; Replication, recombination and repair ;
Unigene21098_tangwq	L138452_1	47.0	8e-06	COG0515	Serine/threonine protein kinase	

RTKL General function prediction only ; Signal transduction mechanisms ; Transcription ;  
Replication, recombination and repair ;  
Unigene63953\_tangwq CAC1728\_1 47.0 8e-06 COG0515 Serine/threonine protein kinase  
RTKL General function prediction only ; Signal transduction mechanisms ; Transcription ;  
Replication, recombination and repair ;